

FIGURE 7

TATTCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCCGATNATCGTCCTCATGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

09078205.104501
105101.5028700

FIGURE 8

GCCCGCGCCCCGGCGCGGGCGCCGGAAGCCGGGAGCCACCGCC**ATG**GGGGCCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCCGCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGATCCCCACCGTCTCTGAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCGCACGGCGGCCTTCTTCTTCT
TCTTTTTACCCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGGCTGCCATCCAG
AATGGGTTTTTGGTTCTTTAAGTTCCTGATCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGCCGAGGAGTGCATTCCTGCGCTGGTACGCAGGCTCTTCTTCTTCACTCTCCTCTT
CTACTTGTCTGCTGATCGCGCCGTGGCGCTGATGTTTCATGTACTACACTGAGCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGGTGTCCATCGCT
GCTGTCTGCCAAGGTCCAGGACGCCAGCCAACTCGGGTCTGTGCAGGCTTCGGTTCAT
CACCCCTCTACACCATGTTTTGTACCTGGTCAAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTTGCCAAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGAGCATTGTGGGCTCATCATCTTCTCCTGTGCACCCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCTGGTGCT
GGCCTCACTGCACGTGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCAGTGGACCGCGCTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGCACTTCAGCT**TG**AGGCAGCCCT
CACAGCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACACGCGTGGAGCTGCCTCTTCTTCCCCTCCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAGGGCTCCTTGTCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACTCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCAGTCCCCAGGGGACCTGCCCCCTTCTTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAAACAGCCAGTGCCTGTAAAAAAA

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE
SPLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWIFYGVVGSFLFILIQLVLLIDFAHSW
NQRWLGAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQOVA
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444